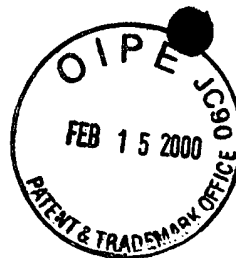SEQUENCE LISTING

(1) GENERAL INFORMATION:

  (i) APPLICANT: Lavi, Sara

  (ii) TITLE OF INVENTION: MANIPULATION AND DETECTION OF PROTEIN
      PHOSPHATASE 2C -PP2CALPHA- EXPRESSION IN TUMOR CELLS FOR
      CANCER THERAPY, PREVENTION AND DETECTION

  (iii) NUMBER OF SEQUENCES: 20

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Kohn & Associates
     (B) STREET: 30500 Northwestern Hwy.
     (C) CITY: Farmington Hills
     (D) STATE: Michigan
     (E) COUNTRY: US
     (F) ZIP: 48334

  (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE:
     (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Kohn, Kenneth I.
     (B) REGISTRATION NUMBER: 30,955
     (C) REFERENCE/DOCKET NUMBER: 2290.00037

  (ix) TELECOMMUNICATION INFORMATION:
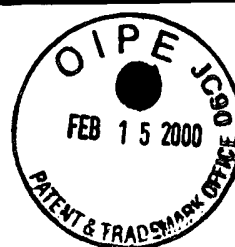   (A) TELEPHONE: (810) 539-5050
     (B) TELEFAX: (810) 539-5055

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 10 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn Asp Asp Thr Asp Ser Ala Ser Thr Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 15 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
1   5   10   15

(2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asn Lys Asp Asn Asp Gly Gly Ala
1   5

(2) INFORMATION FOR SEQ ID NO:4:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGATCAAGT CATAATGGGA   20

(2) INFORMATION FOR SEQ ID NO:5:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 20 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "Primer"

   (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGGAGTCT GATTTACAAC   20

(2) INFORMATION FOR SEQ ID NO:6:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 18 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAGTAGTCG ACACCTGT   18

(2) INFORMATION FOR SEQ ID NO:7:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 21 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTTGAGACC TTCAACACCC C   21

(2) INFORMATION FOR SEQ ID NO:8:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Primer"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGGCCATCT CTTGCTCGAA GTC   23

(2) INFORMATION FOR SEQ ID NO:9:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 6 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ala Phe Leu Asp
1   5

(2) INFORMATION FOR SEQ ID NO:10:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCGC ATGGGAGCAT TTTTAGAC   28

(2) INFORMATION FOR SEQ ID NO:11:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 5 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Asp Asp Met Trp
1   5

(2) INFORMATION FOR SEQ ID NO:12:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 27 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "Primer"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

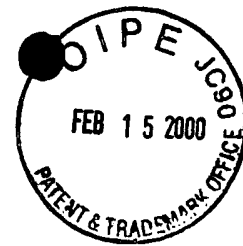CGCGGATCCT TACCACATAT CATCAGT   27

(2) INFORMATION FOR SEQ ID NO:13:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 64 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "Silencer Region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTCCATCAC TAGGGGTTCC TGGAGGGGTG GAGTCGTGAC GTGAATTACG TCATAGGGTT
60

AGGG   64

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "Mini-silencer region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCCCATCA CTAGGGGTTC CT   22

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1573 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "35-3.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTGTCA AAATTACTAT TCAGTGTGAT TTTTAGTGGA TGAAACCTCA TGACTAGTAT
60

ATTATGACAT TAGCTTTGCG TAGTGAAGGC ACAAGCTGCT AAGTGGTTAG GGATGTATTT
120

TGCCGTAGCC TGTATCACNC CAGGTCCTGG GCTCGGTTCC TAGCATTACA GGAAAAAGCA
180

GGCGGTGGTT GACCTTTAAT GAATGGATTT TTCAATTTAG AAGTTGGTTT CATTTTAAAG
240

AATTCAAAAA TGTTCCCCAT AGCACTTTGT TTTGACATTG AGATCAGCTG CTAATTGAGG
300

TCCAGTATAT ACTTAGAAAA CTGAGCGAAA CTTTGATGGA CACACACACA CACCCCTGTT
360

GTTCATTTAA TAATTGAACT AAATAAAATA CTGTTTAGTC ATCCACGTAA GCAAGAGGCC
420

TGTGTAAACA GTATTTGTAT TAGTAAAAAC TTTATAACAT AGTTACATAA TCAGCATCAT
480

TTTTTTTATG GACCTTATAG TTGGCTACTT CACTGGGTTT GTTATAATTT AATCAGACTC
540

CTAAATAGGT TAAATTTCTG AATTGCCTAC TTCAGTTTTG AAGAATTATT TTGTTTCATA
600

ATTTCCCATG CATATCTGGT AAATAATTCT GGATTGTTTC TAAAGGGGAG AGCAAGGTCT
660

CTTATGCAAA GTGAAAATCT AGATATGCTG TTTGTAAGAA TATAATAGTG ATAAAGTAGT
720

GTCCTTTTGC TCAGTGCCTC CATTCTTACC AGGCTGTGAC TGATCTTCAG TATTATTCAG
780

ACAGTCACTA TTAATATATC CGTTGCACAG TGGGGAAATT GAGGGAAGTT AGATAGGCAT
840

CGGGTATCTT AATCATAACT CACATATACC CAGCTGGCTA GTCAGCCTAG CTAAGACAGT
900

TCACACCCAG TTGAGGCAGC TTGCTGTTGG CCATTAGTAG GTAACTTAAT GGCTTGGTTT
960

CTTCACTGGT AAGGTGGGGA TATAATAATG CCAATAATTG CATAATGATT AAAGACATTA
1020

ATATATTCCA TAAAATTTCC TGAATAGTGC TTAGCTGGTA CCCCTCCCCA CACATGCACC
1080

CCAGTCCAAT GTTCAGATGT TTACTTTGTT AAGCCCAGTT AATCCATTCC CCCTAATATC
1140

TTCTCCCAGT TTGAAGAANG TTGAAGAATG TTGGGCTTGT TAGTTTAATT TTTTAAGAAG
1200

CATATCATGT TGCTTTTTTA AAACATGTTT CTTTGGGTTT TGGCTTCCCC TTTTGGAAAG
1260
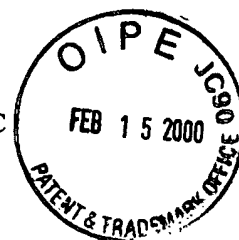
AATTCCAATT TACACTTATG GAAGAAAGCC ATTGTCCCCT CCAATTTCCC CCCCTGTCCC
1320

TTTCCAATAC AGCCCAACTC CCCATGTTTT GACTTCCTCC CCTGAACCAC CCCGTTCTCC
1380

TGTTTTTCCC TCCCCCANAA AAAAAACCCA ATAATTTGAC TTTGGTAATT GAATTTCCCG
1440

CCNGTTAGGC NCCTGAATTG CCGAAATAAT TCCCCCGTGC NCCCNGGANT TTTGGCACCC
1500

CCTGCCCCTT AACCTGTTCT GCTGCCCCCC ATTTTTAAAT GGCTTGCCGC NTTACNCCAA
1560

ANACTGCCTT TCC   1573

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2580 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "35-T7.seg (Figure 3)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCGATCTCA CAAAGTCACA GAGCTCTTCG TTTCCCATGA CATCCCAGAT ACCATCACAT
60

GCAAGAATAA TGAACTGATC GTCCTCTTCA GACCTTTCAA TATCATGGAC TTCTGGCTCT
120

GGTGAGACGA GCTGCTCTGT GGGACCTTTT CCATGGACAC ATTTGTAATC GAAATCCCCA
180

AGGGCCCTTG ACACAGCCAG AGAGCCATTT ACACGCTGAA TCATCACAGA GCCCCCTGCA
240

TTCTGAATTC GTTCTTTTTC CAGCGGGTTA CTTGGTTTGT GGTCTTGTGT GAAGAAGTGA
300

ACTTTCCTGT TTCTACAAAG CAAACCTCTC GAGTCTCCAC AGTTAATGAA GTAAGTATGT
360

TTGGGGAGAA ATTAAGACCC CCACAGCTGT TTGACCCACT TCCTATCTGC ACCATGTTTT
420

CCTTCCTCCT GACATGACTC CTCATGTTGT TTCCATCAAT CTCCCAGAAA AACCTGTTCC
480

TGATCCCCAT TCCTTTACAT TTTCCCACAG AAAGGTGCTC CCTGCAGAGC CTTTTAAAAT
540

CCCTGGTTTA TTGGTGATGT TGATTCTNAA CAAATGCTCC ACAGCCAGTA TTTNGGCAAC
600

CTTGAAAAAC CAGCATGCCC ATCCATATAC AGCCAAGAAT GACCATGTTC TCCAGTTCCA
660

CTTTNGGCAA ACCCAATCCA CAGCCGTTNT GCGCATCCTC CCATTTCAAC TCCGCCCAAC
720

CNTTGCNTGC TGCNTTAAGC CATATCGCAA CCCATCCCCC CTGCCCCCTG GGGCATTATG
780

CNTTTCCATC TTTGGTTGTC TAAAATGCTC CCATTATGAC TTGATCCTCT AGGTCTGCAA
840

AGGAAGAGAA ATAAGAAAGT TAGTAACTGT CTTTGAAACA AAGCACACAT CCAACAGTCT
900

TTTTGAAGCA CCTACGAGAT ACAAGGAAAC GTAAAAACTC ATAGGCTATA GCCATAAGCA
960

TTGTTCTACT GACTTGGAAA ATGTAGAGAT TAATAAGAAA GGGAAAGGCT GATCAAGTAC
1020

AGCTCAACCA GACAAGCAGC AGATGGAACT AAGTCACCAG GTAAAAGAGA GCTTGTTTGC
1080

CTCTCTGTGA TACCAAGGAG GCCCAGCAGT GACCATTAAC TTACATGAAC TAGGCAAGAT
1140

TTCAGGGTGC ATTCATCATA TGTAACCTCT CAATTAAGTT GTGTGTTGAT TAAAAAAAAT
1200

AATTCATAGA AACATACAAG TATCTACTAC TTCAGGGAAC CTTAGCTAAG TACTCAGGAA
1260

TGTTGAGAGT TTGATTCCAT GCTATTTAGT TTTGTTTCTA CAACTAGATA CCTTTGGTAA
1320

AAATAAAAAG TAATTACTCA CACTGGTCCA AATTTTCAGT GCCTTGTGCA GGTCATTCTC
1380

TTTAGCTGGA ATTCCCTGCC TCACCTCTTT ACCAACAGAA AAAAAATACA CCTGTTTCTA
1440

TCCTTTGAAA TCCAGTTCAA TTGTTCCCCC TTCCTCCAGA CTTTACAGTC CTTGAAAAAA
1500

ACAAGTTATT AACTACAGAA GTCAGCTTCC ATTTCCAGTT NGGAATGTTT TTTAATGAAC
1560

AATTTTATTG TTCNAAATCT NACNATATGA TAACTAANCN AATGGTAATA ATATTTTCAN
1620

CCCTGCCCTA TGGCCGCTNT TTTTAATCCT NAAAAAAATC NAAGGTCTAT TCCNCCCNNC
1680

CTTGCCAATA CTTNACANCN CCAGTTCCCT GATCTGGAAT GGACCCACAA AGGTCAAGAC
1740

TTAGGTTANC CCTTGCTCAC AAACTAAAGA AAATCTTAAA GGAGAACAGA ATACTGAAGA
1800

GAGAAATGAG GGTGAAGGAC AGTGTTCAGG TGACGTTCTG AAACCAGGGG ACTAAANATA
1860

CCANAANTGG TGTTNCAGAC AGAAATGGTA TGGAAAACTC CTTAGGAAAG AAATGACANN
1920

TNTTGTTTCG CAGCAACCCC CNCACATGGC TTTCTCTTTT TCCTTCTGCT GATTAACTGA
1980

TGCACNTGGT ANAAAAGTCA ACANACCCCT CCTCCACNCA GACTCCCACC GAGTACANNG
2040

GCCCATGTGC TCANTACACT CTGCCCCAAA CTCNNANNAT TCATTCNNCT CCCCNTGTNA
2100

TTTATNAGGG CCTTTCCCNT CAGTTNTCTN ATCNCCAACG GANATTANCC TTCCANNNAT
2160

TTACCCCCNN TTTGTACANC ACATNNTGGC NNGTGCCACN GTTANGCGTC GGCNTCCCTG
2220

TTNCACTNCA TCCCTCATCN TTAGGCCANG TTTGATTCTC CNGTGCANAN TTTCCGCANN
2280

ANCNTACCCC TTGCACCNTC CATNTCTNNG GAANAACCTC CGGTTCTGAA TCTNCCCCNN
2340

TCCCGTCNCT CCCCCNTTCT TTCTTTTCTC TANTTTTTTC CNNGGNACGG GTTGNGGTNA
2400

ATNAANNCCC CTCCTTCGTC TATTCANCCC TTCCTATGNA CACTTCCTGN CCCCCTATCT
2460

CTCTATNTNC TNCTCTCTAT ATCTNNATCC CNTCTTCNCN TGCCNCTCCC TNGTNTTNNA
2520

NCGGGTATTT NTTNTTCTCC TCNTCTTCTT CCCCTNTNTA NCCNTNCTNC NNNCNNNCCC
2580

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 830 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
       (A) DESCRIPTION: /desc = "5H-1 (Example 10)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGGGAGAG GACTGAAATA TTTCCACAGC CTTTTTATTG GTGGTGATGG TAGTGATGGT
60

TAGGATTCCT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TTTCTTTTTT TTTTTTTTTT   120

TTTTTTTTTT GAGACAGGGT TTCTCTGGGT ACTCCTGGAA CTCACTTTGT GGACCATGAA
180

TGACATGAAT ACTTCGATAT ATACATACAT ACAAAGACAC ATATTTTTAA AAAGAGAATT
240

AGAGTAGAGC TGGGGCAATT GTGGAACACA CCTTTAACCT CAGGCAGATT TCTGCGTTCA
300

AGGTCACCTT GGATTACAAG GCAGCTAGGG CTACACAGAG AAACCATATC TCAAAAAAAA
360

GAAAAAATAA TGAAAGAAAG AAAGGAAGGA AGGAAGGAAG GAAGGAAGGA
AGGAAGGAAG   420

AAAGGAAGGT AGGAAGAAAG GTATTTTCCT AAAAAAAAAA AAAAAAAAAA TTTATTCCGG
480

GCAGTGGTGG CAAATGCTTT TAATCCCACC ATTTGGGAAA GCAGAGGCAG ACAGATTAAA
540

TTTTCAAGGC CCACCTGGTC CTACACAGTG AATTCCAGGA ACACCTAGGT TTACCCANAA
600

AAAACCCCCC CTTGAAATAA ACAAAAATAA ATTAAATAAA TAAAATTTAA AAATAAAACC
660

CGGGCGTTAA ACCCNCTTTT ATCCCCCCAC TTNGGAAGCA AAAGCCGGCN GATTTCTGAA
720

TTCNAGGCCN CCCTGTCTAT GAATTANTTC CCNGAACACC CNAATTTTTC NAAAAACCCC
780

CCNTTTCTTA AAAAANCCAA ATTATTATTN ATTAATTAAA TNAAATTACC   830

(2) INFORMATION FOR SEQ ID NO:18:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 838 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid
     (A) DESCRIPTION: /desc = "AN8T7 (Example 10)"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGTCCAAC AATGGTTTCC ACTTGTCTGG CGGCCGCTCT AGAGTTTCCC ATAAGCTGGA
60

CTGAGAGATG GTGTGATTGC TGTGGGTGAC AAAGACAGAG GCACCTTTCA TCTCTACCCT
120

TCTCTTGTTT TGTTGTTTGT TTGAGACCGG TTCCCACTAT GTAGACCAGG CTGGAGGACA
180

GGGTCTCACT ATGTAGACCA GGCTGGCCTT GAACTCAAAG ACATCTGCCT GCCTCTGCCT
240

CCTGAGGGCT GGGATTAAAG GCGTGTGCTG CCACTGACAG CTTCTATCCT CCTGTCATCA
300

GTCCCGGCTC ACAGGGCCAG AAGATCTCTT CTATGCTTCC ACTATTTCCC CAATCCATTC
360

CCACGGCAGC CTCTCCATCT CCCTACCACC AAGACAGCAG CCTAGTGATA TAACAAAACT
420

TTTATTCACA GGAAACCGGA AAACAAAATC ACAACCAATC ATTTCTATCT AGTCCCTGCC
480

CTAGCCCTCC CTCCAAGCCC CTACATATCC TCCATCTGAG GGGGATGCAT GCGTTGGGTG
540

GGAGCTGCCG GCATCCTTAT CCTGGTTCCT GGAGTAGNGA AGAGTGGTTC TTTTCAACGN
600

CTAGGGNNCT CCCCTCCAAG TTNGGACCTC TCTTCCCAGG NCTTCNCCCC TCCCTNACAG
660

GGNACAAAAA ACCAGGNACG GCACNACGCC AGGNAGGAAG GGACTCTTGG NAATGTTGGG
720

CAGGACTTGT CCTCAGAATT CCNNGGAGGA ATCAAGGGCC TTGAATTCGG GAACCACTNC
780

CGAGGNCTTC ANCANGGCAN AGTTCAATTT TCCATCCCGG TTGGCCCANC CTGGCCNG
838

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 180 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "CHINT (TABLE 5)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGTGCCGGT CAAGGAACTG AACGTGCGAT TCCGGGACAG GCTACCCACT CCGATCCCAG
60

GAGAAGTTGT CATGGTGAGG GCCACCCTAG GTCTCTGCCC CTGCTGTGTC CCCCATCTTA
120

CCCATCCAGT AGGATCTAGA GGCTGTCGCC CCCTTGTGGA ATGCACAGAA GTCACAAGCG
180

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 175 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "HUMMDB (TABLE 5)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCACCTCC GCCCTGTTTC GTCCAGGTCC TCCGGGTCAG GCTACCCCCG TCGCCGCCAG
60

AGCGCGGGGG AGGGGAGAGC TTCCTTTGTC TCCTATGCCT CCTCCCCCCA TCCCGGCTCT
120

CCTGCGGGCA AGCGCCGAGG GGACACCGGG GAGTACCCCA CCTGAACCTC TGGGG
175